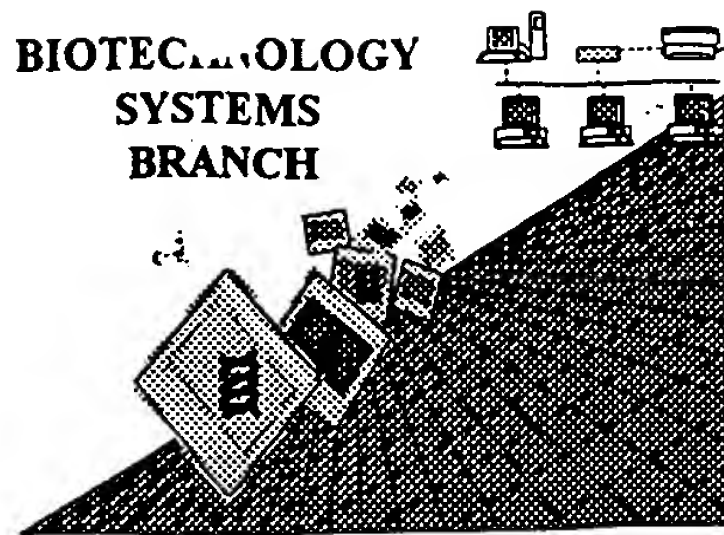


#4

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/765,614A

Source: 1619

Date Processed by STIC: 6/20/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

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Raw Sequence Listing Error Summary

JUL 11 2001

TECH CENTER 1600/2900

SERIAL NUMBER: 09/765,614A

ERROR DETECTED	SUGGESTED CORRECTION
ATTN NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE	
1 <input checked="" type="checkbox"/> <u>Wrapped Nucleics</u> <u>Wrapped Aminos</u>	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/765,614A

DATE: 06/20/2001
TIME: 11:00:39

Input Set : A:\64990SEQ.WPD8-31.txt.txt

Output Set: N:\CRF3\06202001\I765614A.raw

Does Not Comply
Corrected Diskette Needed

pg 1-6

6 <110> APPLICANT: Nycomed Imaging AS
 8 <120> TITLE OF INVENTION: Improvements in or relating to
 9 diagnostic/therapeutic
 10 agents
 12 <130> FILE REFERENCE: REF/Klaveness/054C
 14 <140> CURRENT APPLICATION NUMBER: US/09/765,614A
 15 <141> CURRENT FILING DATE: 2001-01-22
 17 <160> NUMBER OF SEQ ID NOS: 25 31 (p. 6)
 19 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

36 <210> SEQ ID NO: 2
 37 <211> LENGTH: 25
 38 <212> TYPE: PRT
 39 <213> ORGANISM: Artificial Sequence
 41 <220> FEATURE:
 42 <223> OTHER INFORMATION: Description of Artificial
 43 Sequence: Peptide
 44 comprising
 45 phosphatidylserine-binding and
 46 heparin-binding sections

48 <400> SEQUENCE: 2
 49 Phe Asn Phe Arg Leu Lys Ala Gly Gln
 50 Lys Ile Arg Phe Gly Ala Ala
 51 1 5
 52 10 15
 54 Ala Trp Glu Pro Pro Arg Ala Arg Ile
 56 20 25

127 <210> SEQ ID NO: 7
 128 <211> LENGTH: 13
 129 <212> TYPE: PRT
 130 <213> ORGANISM: Artificial Sequence
 132 <220> FEATURE:
 133 <223> OTHER INFORMATION: Description of Artificial
 134 Sequence: Lipopeptide
 135 consisting of a heparin
 136 sulphate binding peptide
 137 and a fibronectin peptide
 139 <220> FEATURE:
 140 <221> NAME/KEY: MOD_RES
 141 <222> LOCATION: (1)
 142 <223> OTHER INFORMATION: Dipalmitoyl-lysine
 144 <400> SEQUENCE: 7
 145 Lys Lys Arg Lys Arg Trp Gln Pro Pro
 146 Arg Ala Arg Ile

move up
 move lines up - Per 1.823
 of sequence rules,
 a MAXIMUM of
 4 lines for <223>
 response

same error

RAW SEQUENCE LISTING

DATE: 06/20/2001

PATENT APPLICATION: US/09/765,614A

TIME: 11:00:39

Input Set : A:\64990SEQ.WPD8-31.txt.txt

Output Set: N:\CRF3\06202001\I765614A.raw

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```

E--> 147      1              5
E--> 148 10
151 <210> SEQ ID NO: 8
152 <211> LENGTH: 24
153 <212> TYPE: PRT
154 <213> ORGANISM: Artificial Sequence
156 <220> FEATURE:
157 <223> OTHER INFORMATION: Description of Artificial
158      Sequence:Fibronectin
159      peptide sequence
161 <400> SEQUENCE: 8
162 Phe Asn Phe Arg Leu Lys Ala Gly Gln
E--> 163 Lys Ile Arg Phe Gly Gly Gly
164      1              5
E--> 165 10              15
167 Gly Trp Gln Pro Pro Arg Ala Ile
E--> 169      20
193 <210> SEQ ID NO: 10
194 <211> LENGTH: 10
195 <212> TYPE: PRT
196 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: Description of Artificial
200      Sequence:Biotinylated
201      fibrin-anti-polymerant peptide
203 <220> FEATURE:
204 <221> NAME/KEY: MOD_RES
205 <222> LOCATION: (1)
206 <223> OTHER INFORMATION: Biotinylated-Gly
208 <220> FEATURE:
209 <221> NAME/KEY: MOD_RES
210 <222> LOCATION: (10)
211 <223> OTHER INFORMATION: AMIDATION
213 <400> SEQUENCE: 10
214 Gly Pro Arg Pro Pro Glu Arg His Gln
E--> 215 Ser
E--> 216      1              5
E--> 217 10
249 <210> SEQ ID NO: 12
250 <211> LENGTH: 18
251 <212> TYPE: PRT
252 <213> ORGANISM: Artificial Sequence
254 <220> FEATURE:
255 <223> OTHER INFORMATION: Description of Artificial
256      Sequence:Endothelial
257      cell binding lipopeptide
259 <220> FEATURE:
260 <221> NAME/KEY: MOD_RES
261 <222> LOCATION: (1)

```

RAW SEQUENCE LISTING

DATE: 06/20/2001

PATENT APPLICATION: US/09/765,614A

TIME: 11:00:39

Input Set : A:\64990SEQ.WPD8-31.txt.txt

Output Set: N:\CRF3\06202001\I765614A.raw

262 <223> OTHER INFORMATION: 2-n-hexadecylstearyl-Lys
 264 <220> FEATURE:
 265 <221> NAME/KEY: MOD_RES
 266 <222> LOCATION: (18)
 267 <223> OTHER INFORMATION: AMIDATION
 269 <400> SEQUENCE: 12
 270 Lys Leu Ala Leu Lys Leu Ala Leu Lys
 E--> 271 Ala Leu Lys Ala Ala Leu Lys
 272 1 5
 E--> 273 10 15
 275 Leu Ala
 312 <210> SEQ ID NO: 14
 313 <211> LENGTH: 13
 314 <212> TYPE: PRT
 315 <213> ORGANISM: Artificial Sequence
 317 <220> FEATURE:
 318 <223> OTHER INFORMATION: Description of Artificial
 319 Sequence:Lipopeptide
 320 with an affinity for
 321 endothelial cells
 323 <220> FEATURE:
 324 <221> NAME/KEY: MOD_RES
 325 <222> LOCATION: (1)
 326 <223> OTHER INFORMATION: Dipalmitoyl-Lys
 328 <220> FEATURE:
 329 <221> NAME/KEY: MOD_RES
 330 <222> LOCATION: (4)
 331 <223> OTHER INFORMATION: Acp
 333 <220> FEATURE:
 334 <221> NAME/KEY: MOD_RES
 335 <222> LOCATION: (13)
 336 <223> OTHER INFORMATION: AMIDATION
 338 <400> SEQUENCE: 14
 W--> 339 Lys Lys Lys Xaa Ile Arg Arg Val Ala
 E--> 340 Arg Pro Pro Leu
 E--> 341 1 5
 E--> 342 10
 345 <210> SEQ ID NO: 15
 346 <211> LENGTH: 14
 347 <212> TYPE: PRT
 348 <213> ORGANISM: Artificial Sequence
 350 <220> FEATURE:
 351 <223> OTHER INFORMATION: Description of Artificial
 352 Sequence:Lipopeptide
 353 comprising an interleukin-1
 354 receptor binding
 W--> 355 peptide
 357 <220> FEATURE:
 358 <221> NAME/KEY: MOD_RES

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TECH CENTER 1600/2900

RAW SEQUENCE LISTING

DATE: 06/20/2001

PATENT APPLICATION: US/09/765,614A

TIME: 11:00:39

Input Set : A:\64990SEQ.WPD8-31.txt.txt

Output Set: N:\CRF3\06202001\I765614A.raw

359 <222> LOCATION: (1)
 360 <223> OTHER INFORMATION: Dipalmitoyl-Lys
 362 <400> SEQUENCE: 15
 363 Lys Gly Asp Trp Asp Gln Phe Gly Leu
 E--> 364 Trp Arg Gly Ala Ala *same*
 365 1 5
 E--> 366 10
 369 <210> SEQ ID NO: 16
 370 <211> LENGTH: 12
 371 <212> TYPE: PRT
 372 <213> ORGANISM: Artificial Sequence
 374 <220> FEATURE:
 375 <221> NAME/KEY: MOD_RES
 376 <222> LOCATION: (1)
 377 <223> OTHER INFORMATION: Dabsyl-Tyr
 379 <220> FEATURE:
 380 <221> NAME/KEY: MOD_RES
 381 <222> LOCATION: (10)
 382 <223> OTHER INFORMATION: RGDS chain linked via NH2 group
 383 of lysine
 385 <220> FEATURE:
 386 <223> OTHER INFORMATION: Description of Artificial
 387 Sequence: Branched core
 388 peptide comprising a dabsylated
 389 atherosclerotic
 W--> 390 plaque-binding sequence and
 W--> 391 RGDS
 393 <400> SEQUENCE: 16
 394 Tyr Arg Ala Leu Val Asp Thr Leu Lys
 E--> 395 Lys Gly Cys *same*
 E--> 396 1 5
 E--> 397 10
 400 <210> SEQ ID NO: 17
 401 <211> LENGTH: 25
 402 <212> TYPE: DNA
 403 <213> ORGANISM: Artificial Sequence
 405 <220> FEATURE:
 406 <223> OTHER INFORMATION: Description of Artificial
 407 Sequence: Synthetic
 408 oligonucleotide
 410 <220> FEATURE:
 411 <221> NAME/KEY: misc_feature
 412 <222> LOCATION: (1)
 413 <223> OTHER INFORMATION: Biotinylated
 415 <400> SEQUENCE: 17
 E--> 416 gaaaggtagt ggggtcgtgt gccgg *see item 1 on Ena Summary Sheet*
 417 25
 419 <210> SEQ ID NO: 18
 420 <211> LENGTH: 15

RAW SEQUENCE LISTING

DATE: 06/20/2001

PATENT APPLICATION: US/09/765,614A

TIME: 11:00:39

Input Set : A:\64990SEQ.WPD8-31.txt.txt

Output Set: N:\CRF3\06202001\I765614A.raw

421 <212> TYPE: PRT
 422 <213> ORGANISM: Artificial Sequence
 424 <220> FEATURE:
 425 <223> OTHER INFORMATION: Description of Artificial
 426 Sequence:Lipopeptide
 427 with affinity for thrombi *thrombin?*
 429 <220> FEATURE:
 430 <221> NAME/KEY: MOD_RES
 431 <222> LOCATION: (1)
 432 <223> OTHER INFORMATION: Dipalmitoyl-Lys
 434 <220> FEATURE:
 435 <221> NAME/KEY: MOD_RES
 436 <222> LOCATION: (15)
 437 <223> OTHER INFORMATION: AMIDATION
 439 <400> SEQUENCE: 18
 440 Lys Asn Asp Gly Asp Phe Glu Glu Ile
 E--> 441 ~~Pro~~ Glu Glu Tyr Leu Gln *same*
 442 1 5
 E--> 443 10 15
 680 <210> SEQ ID NO: 27
 681 <211> LENGTH: 16
 682 <212> TYPE: PRT
 683 <213> ORGANISM: Artificial Sequence
 685 <220> FEATURE:
 686 <223> OTHER INFORMATION: Description of Artificial
 687 Sequence:Atherosclerotic
 688 plaque-binding peptide
 690 <400> SEQUENCE: 27
 691 Tyr Ala Lys Phe Arg Glu Thr Leu Glu
 E--> 692 Asp Thr Arg Asp Arg Met Tyr *same*
 693 1 5
 E--> 694 10 15
 697 <210> SEQ ID NO: 28
 698 <211> LENGTH: 17
 699 <212> TYPE: PRT
 700 <213> ORGANISM: Artificial Sequence
 702 <220> FEATURE:
 703 <223> OTHER INFORMATION: Description of Artificial
 704 Sequence:Atherosclerotic
 705 plaque-binding peptide
 707 <400> SEQUENCE: 28
 708 Arg Ala Leu Val Asp Thr Glu Phe Lys
 E--> 709 Val Lys Gln Glu Ala Gly Ala *same*
 710 1 5
 E--> 711 10 15
 713 Lys
 718 <210> SEQ ID NO: 29
 719 <211> LENGTH: 14
 720 <212> TYPE: PRT

RAW SEQUENCE LISTING

DATE: 06/20/2001

PATENT APPLICATION: US/09/765,614A

TIME: 11:00:39

Input Set : A:\64990SEQ.WPD8-31.txt.txt

Output Set: N:\CRF3\06202001\I765614A.raw

721 <213> ORGANISM: Artificial Sequence
 723 <220> FEATURE:
 724 <223> OTHER INFORMATION: Description of Artificial
 725 Sequence:Thrombus
 726 binding peptide
 728 <400> SEQUENCE: 29
 729 Asn Asp Gly Asp Phe Glu Glu Ile Pro
 E--> 730 Glu Glu Tyr Leu Gln *same*
 731 1 5
 E--> 732 10
 751 <210> SEQ ID NO: 31
 752 <211> LENGTH: 13
 753 <212> TYPE: PRT
 754 <213> ORGANISM: Artificial Sequence
 756 <220> FEATURE:
 757 <223> OTHER INFORMATION: Description of Artificial
 758 Sequence:Platelet
 759 binding peptide
 761 <400> SEQUENCE: 31
 762 Pro Leu Tyr Lys Lys Ile Ile Lys Lys
 E--> 763 Leu Leu Glu Ser *same*
 E--> 764 1 5
 E--> 765 10

PMI
Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
 Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
 <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 06/20/2001

PATENT APPLICATION: US/09/765,614A

TIME: 11:00:40

Input Set : A:\64990SEQ.WPD8-31.txt.txt

Output Set: N:\CRF3\06202001\I765614A.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application Number.
 L:46 M:259 W: Allowed number of lines exceeded, <223> Other Information:
 L:50 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
 M:332 Repeated in SeqNo=2
 L:137 M:259 W: Allowed number of lines exceeded, <223> Other Information:
 L:146 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
 M:332 Repeated in SeqNo=7
 L:163 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
 M:332 Repeated in SeqNo=8
 L:215 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
 M:332 Repeated in SeqNo=10
 L:230 M:259 W: Allowed number of lines exceeded, <223> Other Information:
 L:271 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12
 M:332 Repeated in SeqNo=12
 L:339 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
 L:340 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
 M:332 Repeated in SeqNo=14
 L:355 M:259 W: Allowed number of lines exceeded, <223> Other Information:
 L:364 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:15
 M:332 Repeated in SeqNo=15
 L:390 M:259 W: Allowed number of lines exceeded, <223> Other Information:
 L:391 M:259 W: Allowed number of lines exceeded, <223> Other Information:
 L:395 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
 M:332 Repeated in SeqNo=16
 L:416 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:17
 L:441 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:18
 M:332 Repeated in SeqNo=18
 L:492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
 L:692 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:27
 M:332 Repeated in SeqNo=27
 L:709 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:28
 M:332 Repeated in SeqNo=28
 L:730 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:29
 M:332 Repeated in SeqNo=29
 L:763 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:31
 M:332 Repeated in SeqNo=31
 L:17 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (25) Counted (31)